Remarks

The present invention is related to a novel *Candida albicans* gene, CaNik1, which plays a role in phenotypic switching and, hence, which is correlated to the level of virulence of *C. albicans*. Thus, the present invention relates both to polynucleotides that encode proteins linked to this phenotypic switching and to using such polynucleotides to identify compounds that inhibit phenotypic switching.

Claims 1-20 were pending prior to the present response. By the present response, claims 1, 14 and 15 have been amended to define Applicants' invention with greater particularity. These amendments add no new matter, as they are fully supported by the specification and the original claims. In addition, claims 3, 13 and 17-19 have been cancelled, without prejudice or disclaimer, in an effort to streamline the claims and advance prosecution.

Accordingly, claims 1-2, 4-12, 14-16 and 20 are pending. The Examiner has indicated claims 16 and 20 to be allowable (see Office Action Summary, Paper No. 28). The present status of all claims in the application, and current amendments thereto, are provided in the listing of claims presented herein beginning on page 2.

In response to a requirement by the Examiner, Applicants submit corrected formal drawings under separate cover. A copy of these drawings is enclosed, for the Examiner's convenience.

The objection to claims 17 and 18 under 37 C.F.R. § 1.75(c), as being of improper dependent form for allegedly failing to further limit the subject matter of a previous claim, is respectfully traversed. Applicants submit that "low" and "moderate" stringency conditions indeed are subsets of "stringent conditions" and therefore are in fact of narrower scope that the parent claim. To advance prosecution, however, claims 17 and 18 have been cancelled, rendering this objection moot. Applicants therefore request withdrawal of this objection.

Applicants also respectfully traverse the rejection, under the first paragraph of 35 U.S.C. § 112, of claims 13-15, 17 and 18, which the Examiner contends lack adequate written description. Claims 13, 17 and 18 have been cancelled, without prejudice or disclaimer. Claim 14 and 15 have been amended to

depend from amended claim 1. As to these claims, therefore, this rejection is inapposite, and Applicants respectfully request its withdrawal.

In light of the original specification, one of skill in the art would have no reason to doubt, Applicants submit, that they were in possession of the polynucleotide recited in amended claim 1 and its dependents. Tracking the specification, claim 1 embodies explicit structural requirements for the recited polynucleotide, namely, that it exhibit 70% or greater overall sequence identity to SEQ ID No. 3, the full-length sequence of the exemplary polynucleotide encoding a protein linked to phenotypic switching in *Candida albicans*. Furthermore, amended claim 1 provides explicit functional requirements for the claimed polynucleotide, *i.e.*, it must encode a protein linked to phenotypic switching in *Candida albicans* ***and*** that it must display kinase activity. The specification clearly demonstrates that expression of the full-length sequence is correlated to phenotypic switching, by virtue of the kinase activity of the protein expressed by the full-length sequence. See, for example, Examples 3-5 at pages 17-20.

Moreover, the skilled person readily could envision (and, indeed, could identify with precision) a plurality of sequences embraced by the claims, using only the amino acid sequence of the exemplary protein of SEQ ID NO: 4. By further requiring that the claimed polynucleotide encode a protein with kinase activity, one of skill in the art would know which sequences are associated with this kinase activity, such as the histidine autokinase (H1) domain (encoded by amino acid residues 509-520 of SEQ ID NO: 3, for example).

In keeping with the specification, claim 1 prescribes several identifying characteristics of the claimed polynucleotide, including a combination of structure (sequence) and function (encoding a protein linked to phenotypic switching that has kinase activity). Accordingly, Applicants respectfully submit claim 1 and all claims dependent thereon fully satisfy the requirements of 35 U.S.C. § 112, first paragraph.

The rejection of claims 1-12 and 17-19 under 35 U.S.C. § 112, second paragraph, is respectfully traversed. Applicants submit that these claims as presented are clear to one of skill in the art, because appropriate hybridization conditions were well-known at the time of filing. Applicants need not repeat in the specification what those skilled in the art well know.

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In order to reduce the issues, however, Applicants have amended claim 1, removing reference to hybridization conditions, and have cancelled claims 17-19. Accordingly, they respectfully request reconsideration and withdrawal of this rejection.

The rejection of claims 17 and 18 under 35 U.S.C. § 112, second paragraph, likewise is traversed. As noted, the recitations of low and moderate stringency do not broaden the scope of the parent claims. Also as noted, however, claims 17 and 18 have been cancelled. Accordingly, Applicants respectfully request reconsideration and withdrawal of this rejection.

Conclusion

In view of the above amendments and remarks, prompt and favorable action on all claims is respectfully requested. In the event any matters remain to be resolved in view of this communication, the Examiner is encouraged to call the undersigned so that a prompt disposition of this application can be achieved.

Respectfully submitted,

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Enclosure: Copy of Formal Drawings and Transmittal as filed under separate cover.